

BEST AVAILABLE COPY

Fig. 1

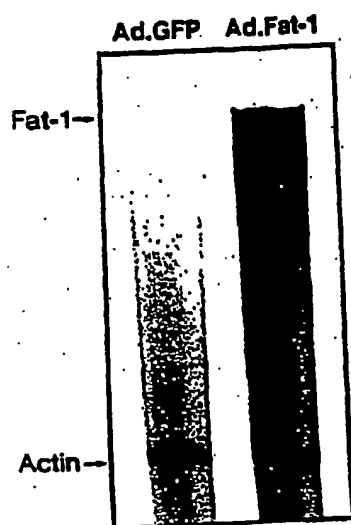


Fig. 2

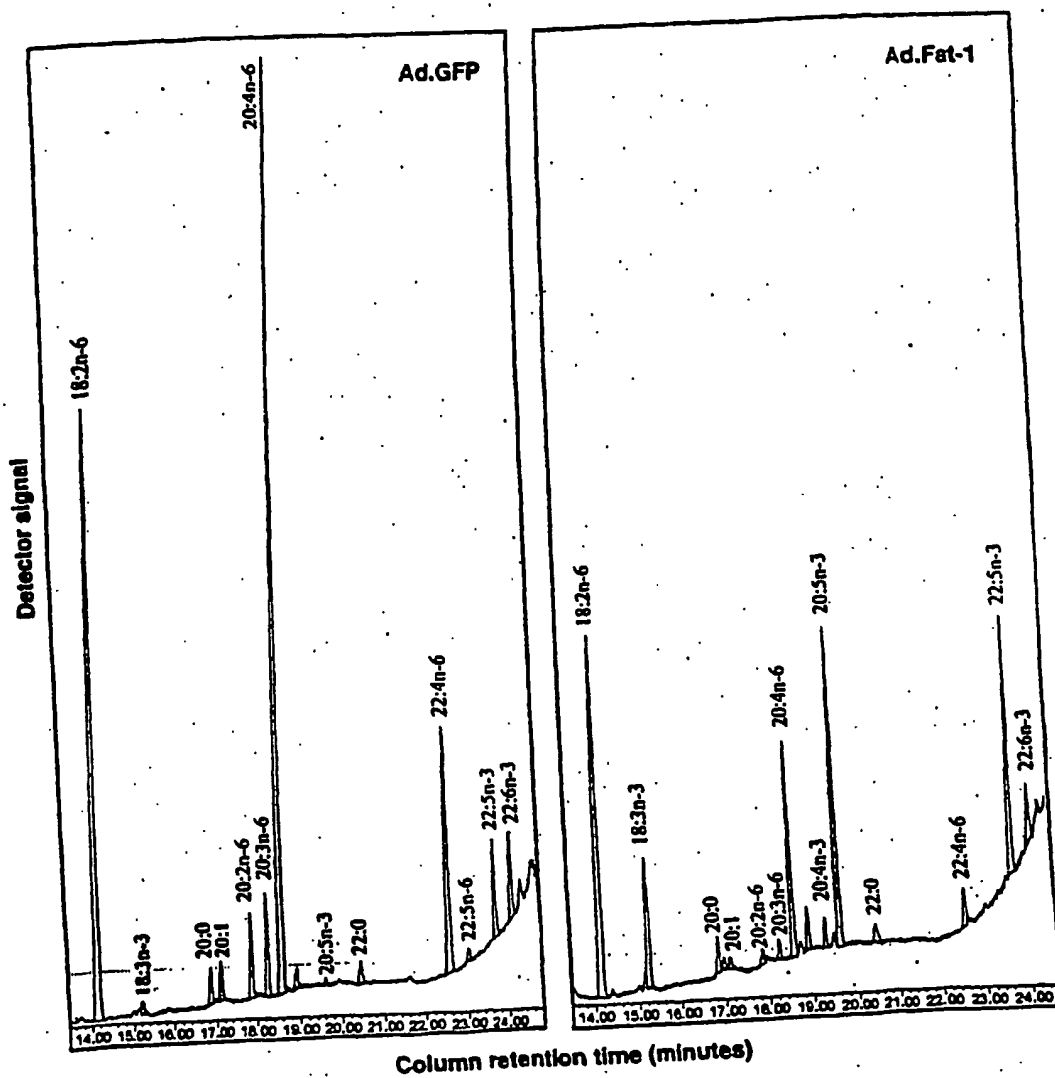


Fig. 3

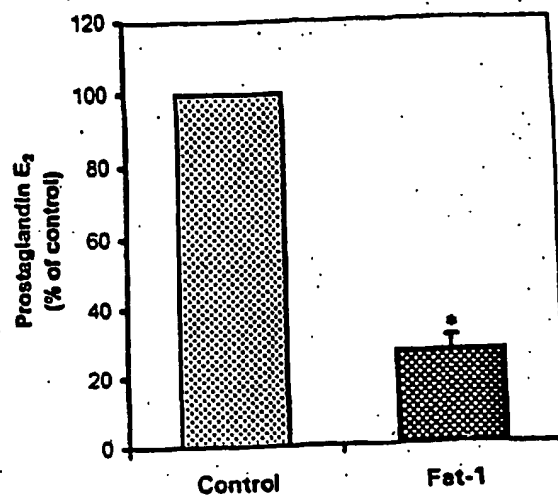


Fig. 4

Mol % of total Fatty acids	Control	Fat-1
n-6 Polyunsaturates		
18:2n-6	14.2 ^a	9.2 ^b
20:2n-6	1.2 ^a	0.3 ^b
20:3n-6	1.6 ^a	0.4 ^b
20:4n-6	15.2 ^a	4.1 ^b
22:4n-6	4.4 ^a	1.0 ^b
22:5n-6	0.2 ^a	0.0 ^b
Total	36.8 ^a	15.0 ^b
n-3 Polyunsaturates		
18:3n-3	0.2 ^b	3.6 ^a
20:4n-3	0.0 ^b	0.6 ^a
20:5n-3	0.1 ^b	6.1 ^a
22:5n-3	1.2 ^b	5.8 ^a
22:6n-3	1.0 ^a	1.3 ^a
Total	2.5 ^b	17.4 ^a
n-6/n-3 Ratio	14.7^a	0.9^b

Values are means of four measurements. Values for each fatty acid with the same letter do not differ significantly ($P < 0.01$) between control and fat-1.

Fig. 5

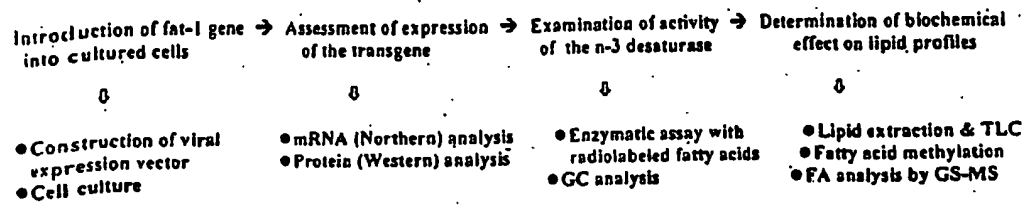


Fig. 6

7/22

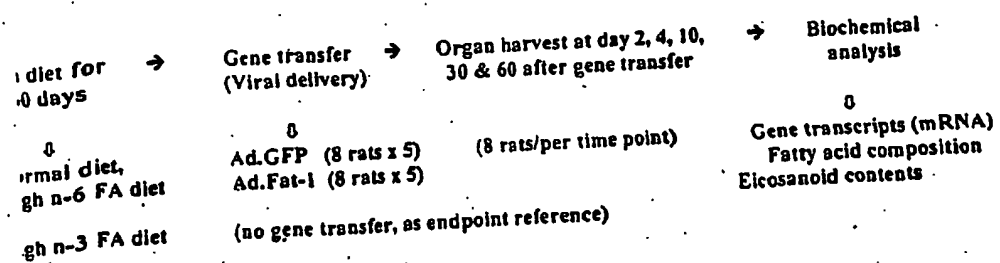


Fig. 7

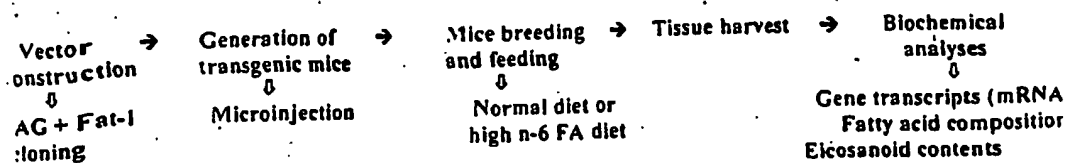


Fig. 8

9/22

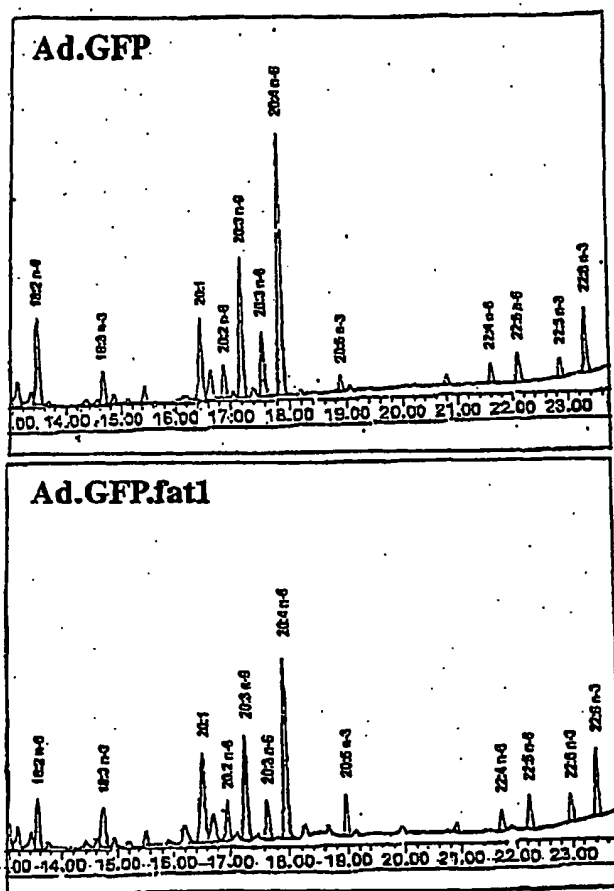


Fig. 9

PUFA composition of total cellular lipids from the
control rat cortical and the transgenic cells expressing a
C. elegans fat-1 cDNA

Mol % of total fatty acids	Control	<i>fat-1</i>
n-6 Polyunsaturates		
18:2n-6	1.78	0.87
20:4n-6	7.21	4.23
22:4n-6	1.57	0.72
22:5n-6	1.68	0.72
Total	12.26	6.53
n-3 Polyunsaturates		
18:3n-3	0.34	0.86
20:5n-3	0.21	0.87
22:5n-3	0.29	0.81
22:6n-3	1.27	1.93
Total	2.11	4.48
n-6/n-3 Ratio	6.44	1.67

Values are means of four measurements. ($p < 0.01$) between
control and *fat-1*.

Fig. 10

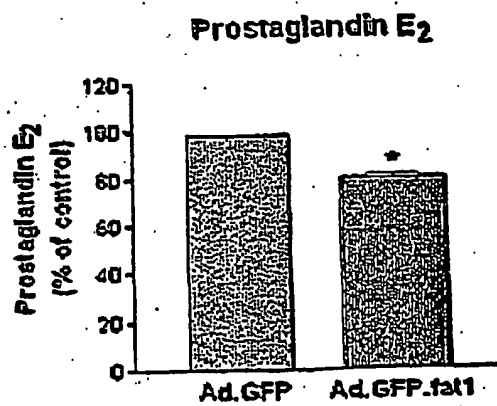


Fig. 11

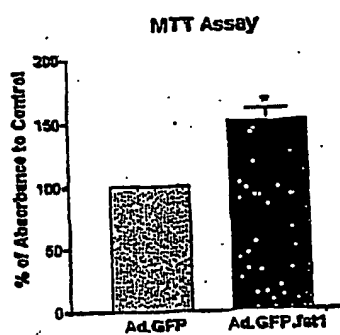
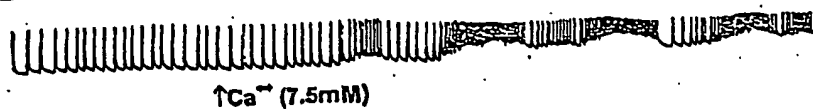


Fig. 12

Ad.GFP



Ad.GFP.Fat-1

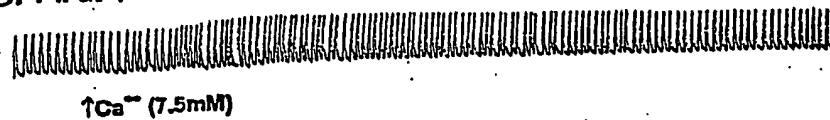


Fig.13

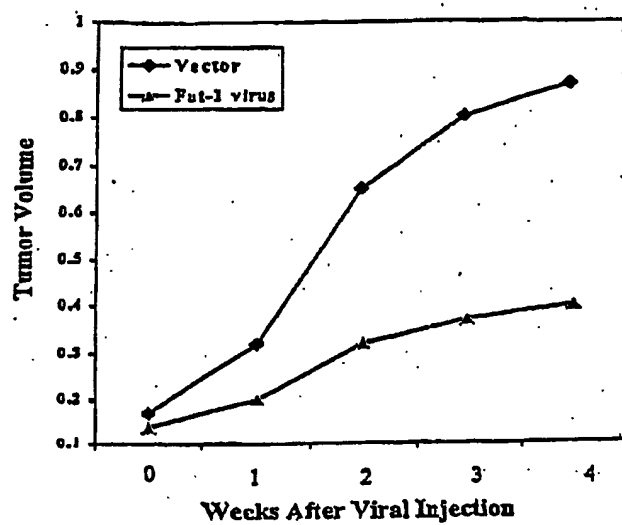


Fig. 14

PUFA composition of total cellular lipids from the control MCF-7 and the transgenic cells expressing a *C. elegans fat-1* cDNA

Mol % of total fatty acids	Control	Fat-1
n-6 Polyunsaturates		
18:2n-6	3.13 ^a	1.51 ^b
20:2n-6	0.23 ^a	0.22 ^a
20:3n-6	0.34 ^a	0.16 ^b
20:4n-6	6.30 ^a	2.26 ^b
22:4n-6	0.53 ^a	0.33 ^b
22:5n-6	0.27 ^a	0.11 ^b
Total	10.80 ^a	4.59 ^b
n-3 Polyunsaturates		
18:3n-3	0.0 ^b	1.00 ^a
20:4n-3	0.0 ^b	0.10 ^a
20:5n-3	0.0 ^b	2.87 ^a
22:5n-3	0.33 ^b	1.47 ^a
22:6n-3	0.60 ^a	0.73 ^a
Total	0.93 ^b	6.17 ^b
n-6/n-3 Ratio	11.61 ^a	0.74 ^b

Values are means of four measurements. Values for each fatty acid with the same letter do not differ significantly ($p < 0.01$) between control and fat-1.

Fig. 15

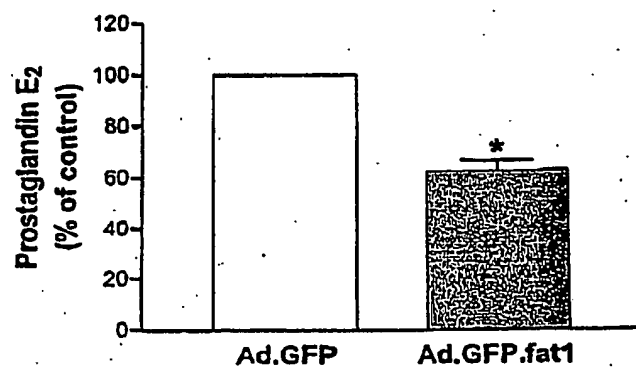


Fig. 1b

17/22

CAAGTTTGAG GT

ATG GTC GCT CAT TCC TCA GAA GGG TTA TCC GCC ACG GCT CCG GTC 57
 Met Val Ala His Ser Ser Glu Gly Leu Ser Ala Thr Ala Pro Val 15
 5 10

ACC GGC GGA GAT GTT CTG GTT GAT GCT CGT GCA TCT CTT GAA GAA 102
 Thr Gly Gly Asp Val Leu Val Asp Ala Arg Ala Ser Leu Glu Glu 30
 20 25

AAG GAG GCT CCA CGT GAT GTG AAT GCA AAC ACT AAA CAG GCC ACC 147
 Lys Glu Ala Pro Arg Asp Val Asn Ala Asn Thr Lys Gln Ala Thr 45
 35 40

ACT GAA GAG CCA CGC ATC CAA TTA CCA ACT GTG GAT GCT TTC CGT 192
 Thr Glu Glu Pro Arg Ile Gln Leu Pro Thr Val Asp Ala Phe Arg 60
 50 55

CGT GCA ATT CCA GCA CAC TGT TTC GAA AGA GAT CTC GTT AAA TCA 237
 Arg Ala Ile Pro Ala His Cys Phe Glu Arg Asp Leu Val Lys Ser 75
 65 70

ATC AGA TAT TTG CTG CAA GAC TTT GCG GCA CTC ACA ATT CTC TAC 282
 Ile Arg Tyr Leu Val Gln Asp Phe Ala Ala Leu Thr Ile Leu Tyr 90
 80 85

TTT GCT CTT CCA GCT TTT GAG TAC TTT GGA TTG TTT GGT TAC TTG 327
 Phe Ala Leu Pro Ala Phe Glu Tyr Phe Gly Leu Phe Gly Tyr Leu 105
 95 100

GTT TGG AAC ATT TTT ATG GGA GTT TTT GGA TTC GCG TTG TTC GTC 372
 Val Trp Asn Ile Phe Met Gly Val Phe Gly Phe Ala Leu Phe Val 120
 110 115

GTT GGA CAC GAT TGT CTT CAT GGA TCA TTC TCT GAT AAT CAG AAT 417
 Val Gly His Asp Cys Leu His Gly Ser Phe Ser Asp Asn Gln Asn 135
 125 130

CTC AAT GAT TTC ATT GGA CAT ATC GCC TTC TCA CCA CTC TTC TCT 462
 Leu Asn Asp Phe Ile Gly His Ile Ala Phe Ser Pro Leu Phe Ser 150
 140 145

CCA TAC TTC CCA TGG CAG AAA AGT CAC AAG CTT CAC CAT GCT TTC 507
 Pro Tyr Phe Pro Trp Gln Lys Ser His Lys Leu His His Ala Phe 165
 155 160

ACC AAC CAC ATT GAC AAA GAT CAT GGA CAC GTS TGG ATT CAG GAT 552
 Thr Asn His Ile Asp Lys Asp His Gly His Val Trp Ile Gln Asp 180
 170 175

AAG GAT TGG GAA CCA ATG CCA TCA TGG AAA AGA TGG TTC AAT CCA 597
 Lys Asp Trp Glu Ala Met Pro Ser Trp Lys Arg Trp Phe Asn Pro 195
 185 190

ATT CCA TTC TCT GGA TGG CTT AAA TGG TTC CCA GTG TAC ACT TTA 642
 Ile Pro Phe Ser Gly Trp Leu Lys Trp Phe Pro Val Tyr Thr Leu 210
 200 205

TTC GGT TTC TGT GAT GGA TCT CAC TTC TGG CCA TAC TCT TCA CTT 687

Fig. 17A

18/22

Phe Gly Phe Cys Asp Gly Ser His Phe Trp Pro Tyr Ser Ser Leu	215	220	225
TTT GTT CGT AAC TCT GAC CGT GTT CAA TGT GTA ATC TCT GGA ATC	732		
Phe Val Arg Asn Ser Asp Arg Val Gln Cys Val Ile Ser Gly Ile	230	235	240
TGT TGC TGT GTG TGT GCA TAT ATT GCT CTA ACA ATT GCT GGA TCA	777		
Cys Cys Cys Val Cys Ala Tyr Ile Ala Leu Thr Ile Ala Gly Ser	245	250	255
TAT TCC AAT TGG TTC TGG TAC TAT TGG GTT CCA CTT TCT TTC TTC	822		
Tyr Ser Asn Trp Phe Trp Tyr Tyr Trp Val Pro Leu Ser Phe Phe	260	265	270
GGA TTG ATG CTC GTC ATT GTT ACC TAT TTG CAA CAT GTC GAT GAT	867		
Gly Leu Met Leu Val Ile Val Thr Tyr Leu Gln His Val Asp Asp	275	280	285
GTC GCT GAG GTG TAC GAG GCT GAT GAA TGG AGC TTC GTC CGT GGA	912		
Val Ala Glu Val Tyr Glu Ala Asp Glu Trp Ser Phe Val Arg Gly	290	295	300
CAA ACC CAA ACC ATC GAT CGT TAC TAT GGA CTC GGA TTG GAC ACA	957		
Gln Thr Gln Thr Ile Asp Arg Tyr Tyr Gly Leu Gly Leu Asp Thr	305	310	315
ACG ATG CAC CAT ATC ACA GAC GGA CAC GTT GCC CAT CAC TTC TTC	1002		
Thr Met His His Ile Thr Asp Gly His Val Ala His His Phe Phe	320	325	330
AAC AAA ATC CCA CAT TAC CAT CTC ATC GAA GCA ACC GAA GGT GTC	1047		
Asn Lys Ile Pro His Tyr His Leu Ile Glu Ala Thr Glu Gly Val	335	340	345
AAA AAG GTC TTG GAG CCG TTG TCC GAC ACC CAA TAC GGG TAC AAA	1092		
Lys Lys Val Leu Glu Pro Leu Ser Asp Thr Gln Tyr Gly Tyr Lys	350	355	360
TCT CAA GTG AAC TAC GAT TTC TTT GCC CGT TTC CTG TGG TTC AAC	1137		
Ser Gln Val Asn Tyr Asp Phe Phe Ala Arg Phe Leu Trp Phe Asn	365	370	375
TAC AAG CTC GAC TAT CTC GTT CAC AAG ACC GCC GGA ATC ATG CAA	1182		
Tyr Lys Leu Asp Tyr Leu Val His Lys Thr Ala Gly Ile Met Gln	380	385	390
TTC CGA ACA ACT CTC GAG GAG AAG GCA AAG GCC AAG TAA	1221		
Phe Arg Thr Thr Leu Glu Glu Lys Ala Lys Ala Lys	395	400	
AAGAATATCC CGTGCCGTTT TAGAGTACAA CAACAACCTT TCGGTTTCA	1271		
CCGGTTTTGC TCTAATTGCA ATTTTTCTTT GTTCTATATA TATTTTTTG	1321		
CTTTTAAAT TTATTCTCTC TAAAAAATT CTACTTTTCA GTGCGTTGAA	1371		
TGCATAAAGC CATAACTCTT	1391		

Fig. 17B

Optimized 1st-4 sequences

1. caa gtt tga ggt ATG gtc gct cat toc AGC gaa ggg Ctg toc ggc aog gct oag gtc aoc
 61. ggc ggc gat gtg ctg gtg gat ggc ogt gca tct ctg gag gag aag gag ggc ooc ogc gac
 121. gtg aat gca aac act aaa cag ggc aoc act gag gag ooc ogc atc caG tta ooc act gtg
 181. gat ggc ttc ogc ogc gca att ooc gca cac tgc ttc gag agG gac ctc gtG aaa tca atc
 241. agG tat Ctg gtg caG gac ttt gog gca ctG aca att ctG tac ttt ggc ctt ooc ggc ttt
 301. gag tac ttt ggC Ctg ttt ggt tac Ctg gtG tgg aac att ttt atg ggC gtt ttt ggC ttc
 361. gog Ctg ttc gtc gtt gga cac gac tgt ctt caC ggC tca ttc toC gat aat cag aat ctc
 421. aat gat ttc att gga cat atc ggc ttc AGC oca ctc ttc tct ooc tac ttc ooc tgg cag
 481. aaa agt cac aag ctG cac caC ggc ttc acc aac cac atC gac aaa gat cat gga cac gtg
 541. tgg atA cag gat aag gat tgg gaa gca atg ooc AGC tgg aaa aga tgg ttc aat oot att
 601. oot ttc tct ggC tgg ctG aaa tgg ttc oot gtg tac act Ctg ttc ggt ttc tgC gat gga
 661. toC cac ttc tgg oot tac toC tca ctG ttt gtG ogC aac tct gaa ogC gtt caG tgt gta
 721. atc tct gga atc tgC tgc tgt gtg tgC gca tat att gct cta aca att gct gga AGC tat
 781. toc aat tgg ttc tgg tac tat tgg gtt oca ctt tct ttc ttc ggC ttg atg ctc gtc att
 841. gtt acc tat Ctg caG caC gtc gac gaC gtc gct gag gtg tac gag gct gat gaa tgg agc
 901. ttc gtc ogG gga caG acc caG acc atc gat ogt tac tat ggC ctc ggC ttg gac aca aog
 961. atg cac cat atc aca gac gga cac gtt ggc caC cac ttc ttc aac aaa atc oca cat tac
 1021. cat ctc atc gaa gca acc gaa ggt gtc aaa aag gtc ttg gag oag ttg toc gac acc caa
 1081. tac ggg tac aaa tct caG gtg aac tac gat ttc ttt ggc ogG ttc ctg tgg ttc aac tac
 1141. aag ctc gac tat ctc gtt cac aag acc gcc gga atc atg caa ttc oga aca act ctc gag
 1201. gag aag gca aag gcc aag tGg aag aat atc oag tgc ogt tct aga gta caa caa caa ctt
 1261. ctg ogt ttt cac ogg ttt tgc tct aat tgc aat ttt tct ttg ttc tat ata tat ttt ttt
 1321. gct ttt taa ttt tat tct ctc taa aaa act tct act ttt cag tgc gtt gaa tgc ata aag
 1381. oca taa ctc tt

Fig. 18

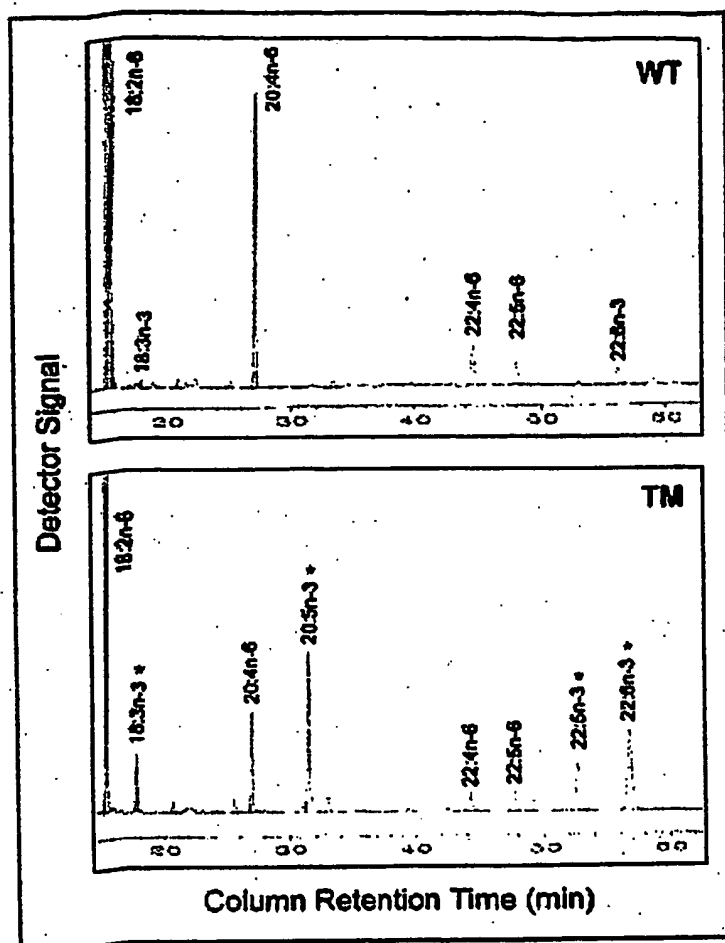


Fig. 19

Fig. 20

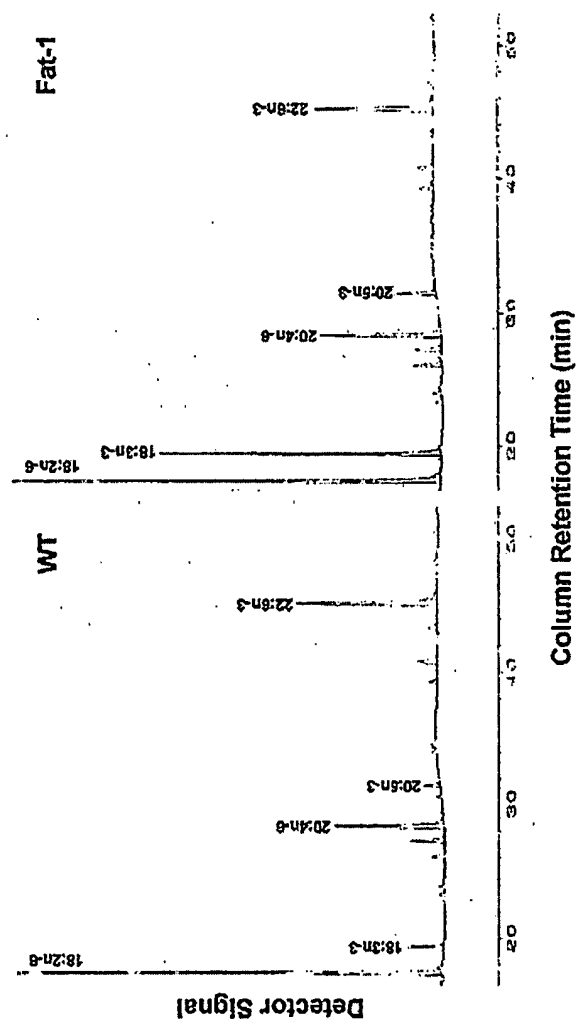
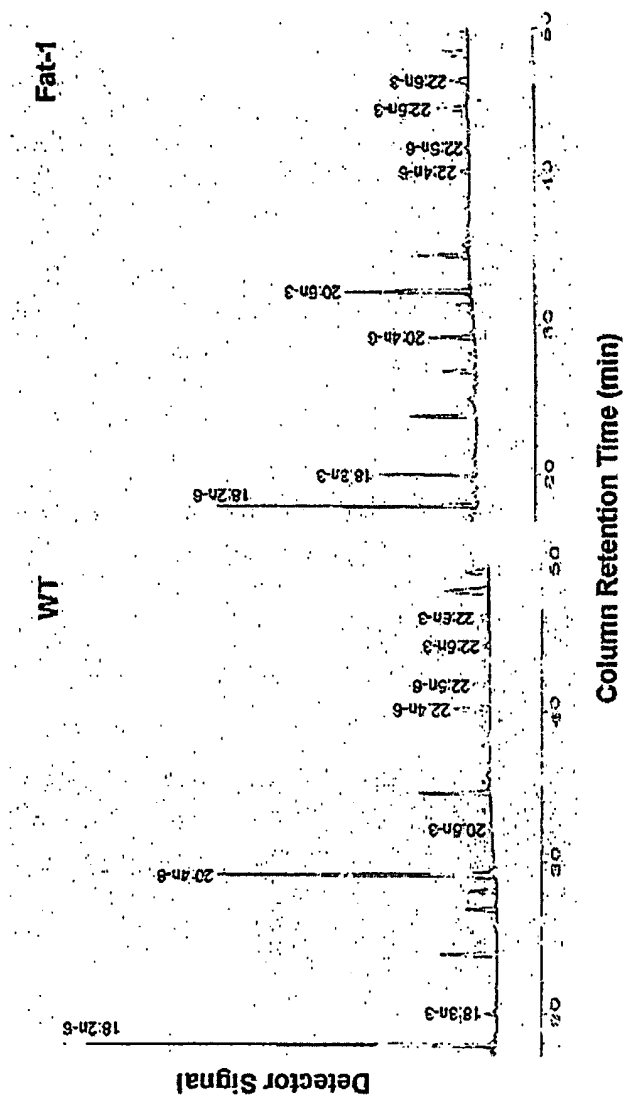


Fig. 21



**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☒ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER: _____**

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.